

Curriculum Vitae

Jason A. Coombs

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Education:

- 2009 **University of Massachusetts**, Amherst, MA
 Ph.D in Organismal and Evolutionary Biology (Expected)
 Dissertation: "Reproduction in the wild: Linking individual life history strategies to lifetime reproductive success"
- 2002 **Clarion University of Pennsylvania**, Clarion, PA
 M.S. in Biology (Emphasis: Aquatic Ecology and Population Dynamics)
 Thesis: "Population structure of brook trout living in adjacent headwater tributaries as revealed by mtDNA analysis"
- 1998 **Lock Haven University of Pennsylvania**, Lock Haven, PA
 B.S. in Biology
 Major: Cellular and Organismal Biology, Minor: Chemistry

Employment:

- 2007-Current **Biological Sciences Laboratory Technician**, U.S. Forest Service, Amherst, MA
- 2002-2007 **Research Assistant**, University of Massachusetts, Amherst, MA
- 2000-2002 **Teaching Assistant**, Clarion University, Clarion, PA,

Related Employment:

- 1998-2000 **Laboratory Technician**, Croda Inc., Mill Hall, PA
 Responsible for quality control of all raw and manufactured chemical products utilizing instrumental analysis and wet chemistry techniques
- 1998 **Laboratory Technician**, Borden's, Wellsboro, PA
 Conducted microbiology testing and assured quality control specifications for food production

Teaching Experience:

- 2008 **Instructor**, UMass, Amherst, MA, Sole developer and lecturer for 200 level required undergraduate course entitled 'Fisheries Management and Conservation'
- Laboratory Instructor**, UMass, Amherst, MA, Responsible for lecturing and creating grading material for laboratory section of undergraduate introductory biology course entitled 'Introductory Animal Biology'
- 2007 **Instructor**, UMass, Amherst, MA, Sole lecturer and laboratory developer for aquatic half of 200 level required undergraduate course entitled 'Animal Sampling and Identification' (Rating 3.9 out of 5.0)
- 2005 **Instructor**, UMass, Amherst, MA, Sole developer and lecturer for graduate level course entitled 'Data Management and Manipulation' which taught the use of Excel, Access and Visual Basic coding (Rating 4.6 out of 5.0)
- 2000-2002 **Teaching Assistant**, Clarion University, Clarion, PA, Instructed laboratories for Genetics, Cellular Biology, and General Biology

Software Development:

All software with the exception of SpawnOpt can be freely downloaded from the website <https://bcrc.bio.umass.edu/pedigreesoftware/>

- CREATE** Creates and converts input files for 57 genetic analysis software programs
- PEDAGOG** Simulates population dynamics while allowing for heritability and selection of traits, and incorporation of demographic and genetic errors
- PEDAGOGGLES** Assesses accuracy and congruence for genetically reconstructed pedigrees, constrains parentage assignment by full-sibling families to improve accuracy
- DistriVIEWtion** Graphs PDF's and CDF's, calculates specific PDF, CDF, and inverse CDF values, and generates samples for thirteen statistical distributions
- 3-In-1** Used for post analysis of simulations from PEDAGOG and parentage assignment comparison output from PEDAGOGGLES
- Colony Extractor** Extracts data from COLONY (Wang, 2004) output files and writes it to a new file in a much more accessible format.
- SpawnOpt** Designed for the U.S. Fish and Wildlife Service for real-time optimization of Atlantic salmon matings for the purpose of minimizing genetic relatedness

Publications:

- Coombs, J.A., Letcher, B.H., and Nislow, K.H. Submitted. PEDAGOG: Software for simulating eco-evolutionary population dynamics. Molecular Ecology Resources.
- Coombs, J.A., Letcher, B.H., and Nislow, K.H. Submitted. PEDAGOGGLES: Software to quantify error and assess accuracy and congruence for genetically reconstructed pedigree relationships. Molecular Ecology Resources.
- Coombs, J.A., Letcher, B.H., and Nislow, K.H. Submitted. DistriVIEWtion: Software for graphing and quantifying probability density functions and cumulative distribution functions for thirteen commonly used distributions. Molecular Ecology Resources.
- Coombs, J.A., Letcher, B.H., and Nislow, K.H. 2008. CREATE: A software to create input files from diploid genotypic data for 52 genetic software programs. Molecular Ecology Resources. 8(3) 578:580.
- Letcher B.H., Nislow K.H., Coombs J.A., O'Donnell M.J., and Dubreuil T.L. 2007. Population response to habitat fragmentation in a stream-dwelling brook trout population. PLoS ONE 2(11) e1139:e1150.

Presentations:

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| 2006 | “The influence of environmental and behavioral processes on lotic brook trout population structure”
American Fisheries Society
Lake Placid, NY September 10-14 |
| 2005 | “Movement biases in both sex and size for Brook Trout during the spawning season”
Ecological Society of America
Montreal, Quebec August 8-12 |
| 2002 | “Using individual based research to evaluate the consequences of movement”
American Fisheries Society
Quebec City, Quebec August 11 - 15 |
| 2002 | “Population structure of brook trout living in adjacent headwater tributaries as revealed by mtDNA analysis”
North American Benthological society
Pittsburgh, PA May 28 – June 1 |